

systems for proteome profiling for example, is of interest. For example, Opiteck and colleagues have published examples of two-dimensional chromatographic systems where fractions eluted from a chromatographic separation system are applied to a second chromatographic system. (See specifically, Opiteck, Lewis and Jorgenson, Anal. Chem, vol. 69, 1518, (1997) which describes the use of a cation exchange system in combination with a reverse phase chromatographic system, and Opiteck et al., Anal Biochem., vol. 258, 349, (1998), which describes the use of size exclusion chromatography in combination with reverse phase chromatography.) The particularly low resolving power of size exclusion chromatography is alleviated in the latter paper by using 8 size exclusion columns in series prior to further fractionation of the eluent by reverse phase chromatography. A theoretical resolving power of 800 proteins was estimated for this system. The limited resolving power of certain chromatographic and electrophoretic systems can also be overcome at the analysis stage. Mass spectrometry is becoming widely used for protein identification following chromatographic or electrophoretic separation and can itself be used as a separation method based on mass. For example, Jensen et al., Anal. Chem. Vol. 71, 2076, (1999) describes the use of capillary isoelectric focusing as a separation method and then use electrospray ionisation Fourier transform ion cyclotron resonance mass spectrometry to further separate proteins in the eluent from the isoelectric focusing system, as well as provide a means of identification.

Brief Description of Drawings Paragraph - DRTX (13):

[0027] FIG. 12 is a graph showing the results of size